

Initial assembled sequence
[Strand]

1 AGAAAATACC CACTTTCTCA GGATGATATC AATGGAATCC AGTCCATCTA TGGAGGTCTG
61 CCTAAGGAAC CTGCTAAGCC AAAGGAACCC ACTATACCCC ATGCCTGTGA CCCTGACTTG
121 ACTTTTGACG CTATCACAAC TTTCCGCAGA GAAGTAATGT TCTTTAAAGG CAGGCACCTA
181 TGGAGGATCT ATTATGATAT CACGGATGTT GAGTTTGAAT TAATTGCTTC ATTCTGGCCA
241 TCTCTGCCAG CTGATCTGCA AGCTGCATAC GAGAACCCCA GAGATAAGAT TCTGGTTTTT
301 AAAGATGAAA ACTTCTGGAT GATCAGAGGA TATGCTGTCT TGCCAGATTA TCCCAAATCC
361 ATCCATACAT TAGGTTTTCC AGGACGTGTG AAGAAAATAG ATGCAGCCGT CTGTGATAAG
421 ACCACAAGAA AAACCTACTT CTTTGTGGGC ATTTGGTGCT GGAGGTTTGA TGAAATGACC
481 CAAACCATGG ACAAAGGGTT CCCGCAGAGA GTGGTAAAC ACTTTCCTGG AATCAGTATC
541 CGTGTTGATG CTGCTTTCCA GTACAAAGGA TTCTTCTTTT TCAGCCGTGG ATCAACGCAA
601 TTTGAATACG ACATTAAGAC AAAGAATATT ACCCGAATCA TGAGAACTAA TACTTGGTTT
661 CAATGCAAAG AACCAAAGAA CTCCTCATTT GGTTTTGATA TCAACAAGGA AAAAGCACAT
721 TCAGGAGGCA TAAAGATATT GTATCATAAG AGTTTAAGCT TGTTTATTTT TGGTATTGTT
781 CATTTGCTGA AAAACACTTC TATTTATCAA TAAATTCATA GACCTAAAAT AAA

Fig. 1

gaaagagagg a atg aag cgc ctt ctg ctt ctg ttt ttg ttc ttt ata aca 50
Met Lys Arg Leu Leu Leu Leu Phe Leu Phe Phe Ile Thr
 1 5 10

ttt tct tct gca ttt ccc tta gtc cgg atg atg gaa aat gaa gaa aat 98
Phe Ser Ser Ala Phe Pro Leu Val Arg Met Met Glu Asn Glu Glu Asn
 15 20 25

gtg caa ctg gct cag gca tat ctc aac cag ttc tac tct ctt gaa ata 146
 Val Gln Leu Ala Gln Ala Tyr Leu Asn Gln Phe Tyr Ser Leu Glu Ile
 30 35 40 45

gaa ggg aat cat ctt gtt caa agc aag aat agg agt ctc ata gat gac 194
 Glu Gly Asn His Leu Val Gln Ser Lys Asn Arg Ser Leu Ile Asp Asp
 50 55 60

aaa att cgg gaa atg caa gca ttt ttt gga ttg aca gtg act gga aga 242
 Lys Ile Arg Glu Met Gln Ala Phe Phe Gly Leu Thr Val Thr Gly Arg
 65 70 75

ctg gac tca aac acc ctt gag atc atg aag aca ccc agg tgt ggg gtg 290
 Leu Asp Ser Asn Thr Leu Glu Ile Met Lys Thr Pro Arg Cys Gly Val
 80 85 90

cct gat gtg ggc cag tat ggc tac acc ctc cct ggg tgg aga aaa tac 338
Pro Asp Val Gly Gln Tyr Gly Tyr Thr Leu Pro Gly Trp Arg Lys Tyr
 95 100 105

aac ctc acc tac aga ata ata aac tat act ccg gat atg gca cga gct 386
 Asn Leu Thr Tyr Arg Ile Ile Asn Tyr Thr Pro Asp Met Ala Arg Ala
 110 115 120 125

gct gtg gat gag gct atc caa gaa ggt tta gaa gtg tgg agc aaa gtc 434
 Ala Val Asp Glu Ala Ile Gln Glu Gly Leu Glu Val Trp Ser Lys Val
 130 135 140

act cca cta aaa ttc acc aag att tca aag ggg att gca gac atc atg 482
 Thr Pro Leu Lys Phe Thr Lys Ile Ser Lys Gly Ile Ala Asp Ile Met
 145 150 155

Fig. 2A

att gcc ttt agg act cga gtc cat ggt cgg tgt cct cgc tat ttt gat	530
Ile Ala Phe Arg Thr Arg Val His Gly Arg Cys Pro Arg Tyr Phe Asp	
160 165 170	
ggt ccc ttg gga gtt ctt ggc cat gcc ttt cct cct ggt ccg ggt ctg	578
Gly Pro Leu Gly Val Leu Gly His Ala Phe Pro Pro Gly Pro Gly Leu	
175 180 185	
ggt ggt gac act cat ttt gat gag gat gaa aac tgg acc aag gat gga	626
Gly Gly Asp Thr His Phe Asp Glu Asp Glu Asn Trp Thr Lys Asp Gly	
190 195 200 205	
gca gga ttc aac ttg ttt ctt gtg gct gct cat gaa ttt ggt cat gca	674
Ala Gly Phe Asn Leu Phe Leu Val Ala Ala His Glu Phe Gly His Ala	
210 215 220	
ctg ggg ctc tct cac tcc aat gat caa aca gcc ttg atg ttc cca aat	722
Leu Gly Leu Ser His Ser Asn Asp Gln Thr Ala Leu Met Phe Pro Asn	
225 230 235	
tat gtc tcc ctg gat ccc aga aaa tac cca ctt tct cag gat gat atc	770
Tyr Val Ser Leu Asp Pro Arg Lys Tyr Pro Leu Ser Gln Asp Asp Ile	
240 245 250	
aat gga atc cag tcc atc tat gga ggt ctg cct aag gaa cct gct aag	818
Asn Gly Ile Gln Ser Ile Tyr Gly Gly Leu Pro Lys Glu Pro Ala Lys	
255 260 265	
cca aag gaa ccc act ata ccc cat gcc tgt gac cct gac ttg act ttt	866
Pro Lys Glu Pro Thr Ile Pro His Ala Cys Asp Pro Asp Leu Thr Phe	
270 275 280 285	
gac gct atc aca act ttc cgc aga gaa gta atg ttc ttt aaa ggc agg	914
Asp Ala Ile Thr Thr Phe Arg Arg Glu Val Met Phe Phe Lys Gly Arg	
290 295 300	
cac cta tgg agg atc tat tat gat atc acg gat gtt gag ttt gaa tta	962
His Leu Trp Arg Ile Tyr Tyr Asp Ile Thr Asp Val Glu Phe Glu Leu	
305 310 315	

Fig. 2B

att gct tca ttc tgg cca tct ctg cca gct gat ctg caa gct gca tac 1010
 Ile Ala Ser Phe Trp Pro Ser Leu Pro Ala Asp Leu Gln Ala Ala Tyr
 320 325 330

gag aac ccc aga gat aag att ctg gtt ttt aaa gat gaa aac ttc tgg 1058
 Glu Asn Pro Arg Asp Lys Ile Leu Val Phe Lys Asp Glu Asn Phe Trp
 335 340 345

atg atc aga gga tat gct gtc ttg cca gat tat ccc aaa tcc atc cat 1106
 Met Ile Arg Gly Tyr Ala Val Leu Pro Asp Tyr Pro Lys Ser Ile His
 350 355 360 365

aca tta ggt ttt cca gga cgt gtg aag aaa ata gat gca gcc gtc tgt 1154
 Thr Leu Gly Phe Pro Gly Arg Val Lys Lys Ile Asp Ala Ala Val Cys
 370 375 380

gat aag acc aca aga aaa acc tac ttc ttt gtg ggc att tgg tgc tgg 1202
 Asp Lys Thr Thr Arg Lys Thr Tyr Phe Phe Val Gly Ile Trp Cys Trp
 385 390 395

agg ttt gat gaa atg acc caa acc atg gac aaa ggg ttc ccg cag aga 1250
 Arg Phe Asp Glu Met Thr Gln Thr Met Asp Lys Gly Phe Pro Gln Arg
 400 405 410

gtg gta aaa cac ttt cct gga atc agt atc cgt gtt gat gct gct ttc 1298
 Val Val Lys His Phe Pro Gly Ile Ser Ile Arg Val Asp Ala Ala Phe
 415 420 425

cag tac aaa gga ttc ttc ttt ttc agc cgt gga tca acg caa ttt gaa 1346
 Gln Tyr Lys Gly Phe Phe Phe Phe Ser Arg Gly Ser Thr Gln Phe Glu
 430 435 440 445

tac gac att aag aca aag aat att acc cga atc atg aga act aat act 1394
 Tyr Asp Ile Lys Thr Lys Asn Ile Thr Arg Ile Met Arg Thr Asn Thr
 450 455 460

tgg ttt caa tgc aaa gaa cca aag aac tcc tca ttt ggt ttt gat atc 1442
 Trp Phe Gln Cys Lys Glu Pro Lys Asn Ser Ser Phe Gly Phe Asp Ile
 465 470 475

Fig. 2C

aac aag gaa aaa gca cat tca gga ggc ata aag ata ttg tat cat aag 1490
 Asn Lys Glu Lys Ala His Ser Gly Gly Ile Lys Ile Leu Tyr His Lys
 480 485 490

agt tta agc ttg ttt att ttt ggt att gtt cat ttg ctg aaa aac act 1538
 Ser Leu Ser Leu Phe Ile Phe Gly Ile Val His Leu Leu Lys Asn Thr
 495 500 505

tct att tat caa taaattcata gacctaaaat aaacctcaac aggtcttttta 1590
 Ser Ile Tyr Gln
 510

atataaattc tgcttcaaaa tagaataaaa ccattcttta acaacaagtt gctggtccta 1650
 gttctaaata tccaaattca atggccattt tgagctgcct gattctttta ataggaagtt 1710
 attatgtaga aacaaaaatc tctgactgta cttaagcct atttcatgct ttgtggactt 1770
 ggagaagaca tgtcttataa ctgaatactg aaacatttat taaaccaatc ttttagcattc 1830
 tg 1832

Fig. 2D

Leader Peptide

1	M---	K---	RLLLFLFFITSSAFPLVR---	MM---	E-----	NEENVQL-AQAYLNQFYSLIEGHNHLVQSK-NRSLIDDKIREMQ	contig 355 long
1	HSFP-----	P---	L	WGVV.HS..ATL---	ET---	QEQ-DV-----D..V.K..EKY.N.KND.RQVEKRR-.SGPVVE.LKQ..	contig 355 short
1	FSL-----	T.PF.L.LHVQI.K....	V---	SS---	KEK-NT-----	KT-V.D..EK.Q.PSNQVQSTRKN-GTNV.VE.LK...	COLL1HUM.PRO
1	HPGV-----	LAAF...	SWTH-CR.L..PS---	GG---	DED-DLS..DL.F-.ER..RSY.H-PTNLAGILKEN-AA.SMTERL....		COLL2HUM.PRO
1						TV.CAV-CLLPGSLA.PL---	COLL3HUM.PRO
1						PQ---	MATRUM.PRO
1						AG-GMS.LQWEQ-.D..KR..LYDS.TKNA-----NSLEA.LK...	METAHUM.PRO
1						F..IL.LQA.A.G.L..NS---	STO1HUM.PRO
1						ST---	STO2HUM.PRO
1						S.PI.L.LCVAVC..Y..DG--AA--RGE-DTS--MN..V.K..ENY.D.KDVQKF.RR..-DSGPVVK....	STO3HUM.PRO
1						M-----H.AF.V.LCLPVC..Y..SG--AA--KEE-DS..-KD..-Q..EKY.N..KDVQKF-RR..-DSN..VK..QG..	MTM1HUM.PRO
1						APAAW-----LRSAAAR.LLPPMLLLL-----QPPPL.AR--A.PPDVH..HAERRGPQPIHAAALPSSP	MTM2HUM.PRO
1						SPAPRPP-----RCLL.PLLTLGTALASLG---SAQSSFSPE.W.Q.YGY.PPGDLRHTHTQR-SPOQSLAA.AA..	MTM3HUM.PRO
1						GSDPSAPGRPGWTGS.LGDREEAARPL..PLLLV--LLGCLGLGVA.A.DAEVH.ENW.RLYGY.PQPSR.MSTM-SAQILASALA...	MMP 17P
1						ILLTFSTGRR-----LD.VHSG-----VFFLQTLWLILCATVCGTEQYFNVEVW.QKYGY.PPTDPRMSVVR-SAETMQSALAA..	MMP 18P
1						QQFGG-----LEA.G-----I-----DEATL-----	MMP 20P
1						NCQQLWLG-----FLLP.TVSGRVLGLA.----VAPVD..S.YGY.QKPLE--GSNNFKPED.TEAL.AF.	MMP 21P
1						HPGV-----LAAF...SWTH-CR.L..PS---GG---DED-DLS..DL.F-.ER..RSY.H-PTNLAGILKEN-AA.SMTERL....	MMP 22P
1							GELAHUM.PRO
1						GRGARVPS-----EAPGAGV.RRW.G.A--VALCL.PA---LVLLARLGAPAVPAW-----	GELBUM.PRO
1						EALMARGALTGP.RA.C.LGCLL.H.AAAPS---PIIKFPGD-VAPKTDKE..-VQ...T..GCPK.SCN.-----FVLK.TLKK..	
1						---SLWQPL---V.V.LVLGCC.AAPRQRQS---TLVLFPGDLRT.LTDR..-EE..YRY-----GYTRVAEMRGESKSLGPALLLL..	

Cystine switch

68	AFFGTLVTGRLDSENTLEIMKTPRCGVPD-----	VGQYG-----	Y--	TLPGWRKYNLT	TYRIINT--	PDMAAAVDEAIQEGLEWWSKVT	contig 355 long
68							contig 355 short
69	E...K...KP.AE.KV.Q.....	A.FV-----	LTEGN.R.EQTH....	E....	LP.D.H.EKAFQL.N..		COLL1HUM.PRO
68	R...N...KPNEE.DM.K.....	S.GFM-----	LTPGN.K.ERT....	R....	QLSE.E.ER..KDAF.L..VAS		COLL2HUM.PRO
73	S....E...K.D..DV.K.....	E.N-----	VFPRTLK.S.M.....	V....	THSE.EK.FKKAFAK...D..		COLL3HUM.PRO

Fig. 3A

64 K...PI..M.N.RVI...QK.....AE.S-----LFPNS.K.TSKW...VS.--R.LPHIT..RLVSKA.NM.G.EI MATRHUM.PRO
69 H.L.K...Q.TS..M.HA.....HFR-----EMPGG.V..HYI...N...N.ED..Y..RKAQF...N.. METAHUM.PRO
69 K.L.E...K.D..V.RK.....HFR-----TFPGI.K...TH...V...LPKD...S.VEKA.K.EE.. STO1HUM.PRO
68 K.L.E...K.TD..V.RK.....HFS-----SFGPM.K...TH...V...LP.D...S..EKA.K.EE.. STO2HUM.PRO
60 ---APATQEAAPRASSLRP.....PSDGLSA---RNRQKRFVLSGGR.E.TD.....LRFPW--QLVQEQ.RQTMA.A.K...D.. STO3HUM.PRO
70 K.Y.Q...KA.AD.MKA.RR.....KFGAEIKANVRR--KR.AIQGLK.QHNEI.FC.Q...--KVGEY.TY...RKAFR..ESA. MTM1HUM.PRO
88 R.Y.IP...V.EE.K.W..R.....QFGVRVKANLRRRKR.AL.GRK.NNH..FS.Q...--EKLGWYHSM..VRRAFR..EQA. MTM2HUM.PRO
78 Q.Y.INM..KV.R.IDW..K.....Q--TRGSSKFHRRKR.AL.GQK.QHKHI..S.K.V.--KVGDPETRK..RRAFD..QN.. MTM3HUM.PRO
19 -----AL.....SL..-LPVLTQ---ARRRQ-APATK.N.R..SW.VRTFPRDSPLGHD.T.RALMYA.K...DIA MMP 17P
62 EASE.P.S.Q..DA.RAR.RQ...LE.P-----FNQKTLK.LLLG-R...KH..F..L.LP--STLPPHTARA.LRQAFQD..N.A MMP 18P
73 S...E...K.D..DV..K.....E.N-----VFPRTLK.S.M.....V...THSE.EK.FKAKF...D.. MMP 20P
7 -----AT.RK...SL..VLGVAGL---VRRRRR.ALGSV.K.RT..W.VRSFPOSSQLSQET.RVLMSYA.MA.GMES MMP 21P
49 -----SAAQGVAA.GLSAV.PTR..GPLAP-----RRRRYTLTPARLR.DHL.....LSFPRNL-LSPRETRR.LAAAFRM..D.S MMP 22P
79 K...PQ..D.Q..I.T.RK...N.....AN.N-----FFPRK.K.D.NOI.....G...LDPET..D.FARAFQ...D.. GELAHUM.PRO
76 KQLS.PE..E...A.KA.R.....-L.RFQ-----TFEGDLK.HHH.I..W.Q..S-E.LP..VI.D.FARAFAL..A.. GELBHM.PRO

Second Zn++ and Ca++ binding domain

143 PLKFTKI-----SKGIADIMIAFRTRVHGRC-----PRYFDGPLGLVGHAFPPGPG-LGGDTHFDEDENWTKDGA----- contig 355 long
143-----
146 ..T..V-----E.Q...S.VRGD.RDN-----SP-...G.N.A..Q...-I..A.....R..NNFR----- contig 355 short
145 ..I..R-----Q.E..N..YQ.D.DN-----SP-...N.I.A..Q..Q.-I..A...AE.T..NTS.----- COLL1HUM.PRO
150 ..N..RL-----HD...S.GIKE..DF-----YP-...S.L.A.....N-Y..A..D..T..SSSK----- COLL2HUM.PRO
141 ..H.R.V-----VW.T...G.ARG.A.DS-----YP-...GNT.A..A..T...A.....R..DGSSSLGIN----- COLL3HUM.PRO
146 ...S.....NT.M..LVV.ARG.A.DF-----HA-...KG.I.A..G..S.-I..A.....F..THSG----- MATRHUM.PRO
146 ..T.SRL-----YE.E...S.AV.E.DF-----YP-...GN..A..YA...IN..A..D..Q...TT----- METAHUM.PRO
145 ..T.SRL-----YE.E...S.AVKE..DF-----YS-...GHS.A..Y...-Y..I..D..K..E.AS----- STO1HUM.PRO
142 ..T.E-----V---HE.R...D.ARYWD.DD-----LP-...G.I.A..F.KTHR-E..V..Y..T..IG--D----- STO2HUM.PRO
156 ..R.REVPYAYIREGHEKQ.....F.AEGF..DS-----TP-...EG.F.A..YF..N-I.....SA.P..VRNEDL----- STO3HUM.PRO
MTM1HUM.PRO

Fig. 3B

TABLE 3

176	.V.QEVPYEDIRLRQKE...	VL.ASGF.DS	SP	TG.F.A.YF	A.P.FSSTD	MTM2HUM.PRO			
164	.T.EEVPYSELENGK-RDV...	P.I.ASGF.DS	SP	EG.F.A.YF	S.P.LGNPNH	MTM3HUM.PRO			
88	.N.HE	VA	GST	Q.D.SKAD.NDG	YP	G.TVA.F.HHHTA	D.A.FRSSD	MMP 17P	
141	.T.QEV	QA.A	RLS.HG.QSSY	SNT	GR.A.DI.EL	SV	F.EGT	MMP 18P	
150	.N.RL	HD	S.GIKE.DF	YP	S.L.A	N.Y.A	D.T.SSSK	MMP 20P	
78	G.T.HE	VDSPQGE	P.L.D.ARAF.QDS	YP	LG.T.A	F.EHPIS	DE.T.FGSKA	MMP 21P	
126	.FS.REVA	PEQPS	LR.G.YPIN.TD	LVSALHHC	T.E.A	F.PH	GI	DS.Y.VLGPTR	MMP 22P
156	.R.SR	HD.E	N.GRWE.DG	YP	KD.L.A	A.T.V	S.D.L	L.GEGQVVRVKYGNADG	GELAHUM.PRO
153	.T.RV	YSRD	V.Q.GVAE.DG	YP	KD.L.A	IQ.A	D.L	SLGKGWVPTFRGNADG	GELBHM.PRO
206								contig 355 long	
263								contig 355 short	
208								COLL1HUM.PRO	
207								COLL2HUM.PRO	
212								COLL3HUM.PRO	
208		FLYA						MATRUM.PRO	
208								METAHUM.PRO	
208								STO1HUM.PRO	
207								STO2HUM.PRO	
203								STO3HUM.PRO	
228								MTM1HUM.PRO	
248								MTM2HUM.PRO	
235								MTM3HUM.PRO	
152								MMP 17P	
201							YR	MMP 18P	
212								MMP 20P	
145								MMP 21P	

Fig. 3C

194	-----Ysw-----	MMP 22P
231	EYCKFPFLFNGKEYNSCTDGRSDGFLWCSTTYNFEKDKYGFPCHEALFTMGNAEQCKPFRFQGTSDCTTEGRTDGYRWCGTT	GELAHUM.PRO
228	AACHFPFIFEGRSYSACTTDGRSDGLPWCSTTANYDTRDFGFCPSERLYTRDGNADGKPCQFPETIFQGQSYSACTTDGRSDGYRWCAAT	GELBHUM.PRO
207	-----GFNLFLVAHEFGHAL	contig 355 long
164	-----	contig 355 short
209	-----EY.HR....L.S.	COLL1HUM.PRO
208	-----NY.....S.	COLL2HUM.PRO
213	-----Y.....S.	COLL3HUM.PRO
212	-----T.L.L.S.	MATRUM.PRO
209	-----T...T.V.I.S.	METAHUM.PRO
209	-----T.....I.S.	STO1HUM.PRO
208	-----T.....L.S.	STO2HUM.PRO
204	-----DQ.TD.LQ.....V.	STO3HUM.PRO
229	-----N.NDI...V.L....	MTM1HUM.PRO
249	-----H.N.....V.L....	MTM2HUM.PRO
236	-----D.ND....V.L....	MTM3HUM.PRO
153	-----AH.MD..A.V.....I	MMP 17P
203	-----V.RII....V....	MMP 18P
213	-----Y.....S.	MMP 20P
146	-----SQGLE-----Q.LAGG-	MMP 21P
197	-----KKGW-----LTD.VH....I....	MMP 22P
321	EDYDRDKKYGFCPETAMSTV-GGNSEGAPCVFPFTFLGNKYESCTSAGRSDGKMGWCAATANYDDDRKMGFCPDQ.YS.....M	GELAHUM.PRO
318	ANYDRDKLFGFCPTRADSTVMGNSAGELCVFPFTFLGKEYSTCTSEGRDGLWCATTSNFDSDKKMGFCPDQ.YS.....	GELBHUM.PRO

Fig. 3D

FIG. 3E

Zn++ binding domain			
223	GLSHNDQTALMFPNYVS-L-DPRKYPLS--QDDINGIQSIYGG-----LPKEPAKPEPTIP-----		contig 355 long
180		contig 355 short
225T.IG...Y.S.-T-F--SGDVQ.A--...D...A...RSQNPVQ-----IG.QT.		COLL1HUM.PRO
224A..S.PG...Y...-A-FRETSN.S.P--...D...A...LSSNPIQ-----TG.ST.		COLL2HUM.PRO
229D..K.PG...I..-T-YTGKSHFM.P--D..VQ...L..PGDE-----DPN..H.KT.		COLL3HUM.PRO
221MG..S.PN.V.Y.T.-G-NG..QNFK...K..KL.		MATRUM.PRO
225G..S.PK.V...T.K--YV.INTFR.--A...R...L..DPKENQRLP-----NPDNSE.		METAHUM.PRO
225F..ANTE...Y.L.H.-.T.LTRFR.....L..PPDSPETP.VTEPV.P..GT.		STO1HUM.PRO
224F..ANTE...Y.L.N.-FTELAQFR.....V...L..PPASTEETP.VPTKSV.SGSEM.		STO2HUM.PRO
222Q..TTAAK...SAF.....TFR...LSP..CR.V.HL..QP--WPTVTSRT-----		STO3HUM.PRO
246E..S.PS.I.A.F.Q--WM.TENFV.P--D..RR...QL...ESG-----FPTKM.PQ.-RT-SRPSVPDKPKNPT-----		MTM1HUM.PRO
266E..SNPN.I.A.F.Q--WK.VDNFK.P--E..LR...QL..TPDGQPQTQ.LPTVT.RR.GR.-DHRPPRPQPPPGGKPERPPKP		MTM2HUM.PRO
254E.....P..I.A.F.Q--YME-QTLQ.P--N..YR--HQR.MSPDKIPPTR.LPTV.-PHRS.-PADPRKNDRKPPRPPTGRPSYP		MTM3HUM.PRO
171VAAAHSI.R.Y.QGPVG..LR.G.PYE-.KVR-VWQL..VRESVSPTAQ.E.		MMP 17P
219G..RYSQ...A.V.EG--YRPHFK.H--P..VA...AL..KKSPVIRDEEEE.TEL.TV.PV.TEPS-----		MMP 18P
229D..K.PG...I..-T-YTGKSHFM.P--D..VQ...L..PGDE-----DPN..H.KT.		MMP 20P
157PVDEELGFS-----		MMP 21P
218M..QHGR.....-H.NATLRGKALS..ELW.LHRL..C-----LDRLFVCASWARRGF-----		MMP 22P
410E..Q.PG...A.I.-T-YT--KNFR.....K...EL..ASPD--ID.GTG.TPTLG.VT.		GELAHUM.PRO
408D..SVPE...Y.M.R--FTEGP--H--K..V...RHL..PRPEPRPPTTTTPQ.TA.PTVCPTGPPTVHPSERPTAGTGPSPA		GELBHUM.PRO
277	-----HACD--PDLTFDAITTFREVWFFKGRHLWR-IYYDITDVE-FELIASFWPSLP---ADLQAAYENP-		contig 355 long
234	-----		contig 355 short
276	-----K....SK.....I.G.....D.FYM.-TNPFFE..LNF.SV...Q....NG.E....FAD		COLL1HUM.PRO
277	-----KP...S....S.....L.G.IL..D.YF..RHPQLQR..-MNF.SL.....TGI.....DFD		COLL2HUM.PRO
282	-----DK...S.SL....SL.G.T.I..D.FF..-LHPQQV.A.-LF.TK...E....NRID....H.S		COLL3HUM.PRO
259	-----		MATRUM.PRO

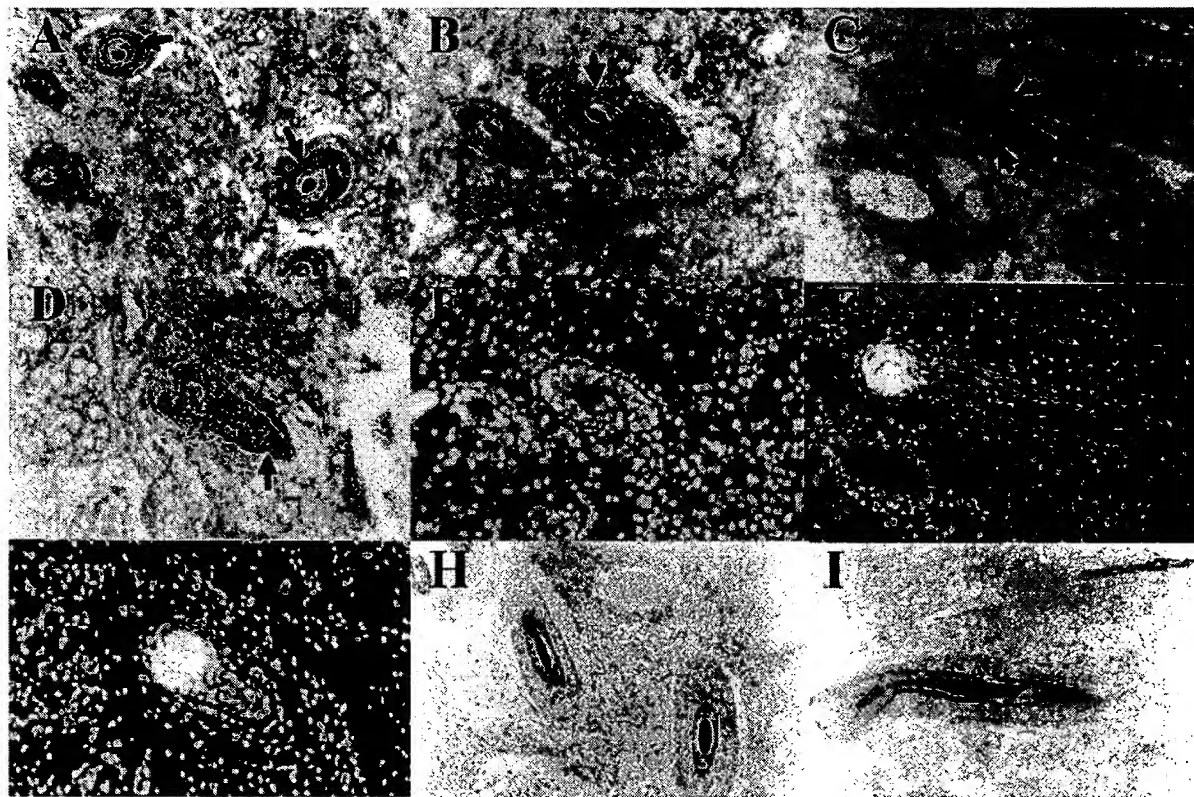
Fig. 3E

102040" 05110850

280	-----AL.---.N.S...V..VGNKIF...D.FF.L-KVSRPKTS-VN..S.L..T.---SGIE....IEA	METAHUM.PRO
288	-----AN.---.A.S...VS.L.G.ILI..D..F..-KSLRKLEP..-LH..S.....-SGVD....VTS	STO1HUM.PRO
287	-----AK.---.A.S...S.L.G.YL..D.YF..-RSHWNEP..-H..SA.....-SY.D....VNS	STO2HUM.PRO
269	-PALGPQAGIDTNEIAPLEDPAPDA--CEAS...VS.I.G.LF..AGFV..L-RGGQLPGYPA.ASRH.QG.---SPVD..F.DAQ	STO3HUM.PRO
314	-----YGP-----NI.---GN--..TVAML.G.MFV..E.WF..VRNQVM.GYMPM--GQ..RG.---SINT...RKD	MTM1HUM.PRO
351	GPPVQPRATERPDQYGP-----NI.---G.---TVAML.G.MFV...WF..VRHNRVL.NYPMP--GH..RG.---G.IS....RQD	MTM2HUM.PRO
334	GAK-----P-----NI.---GN--..NTLAIL...MFV..DQWF..VRNRMV.GYPMQ--TY..RG.---PSID.V...SD	MTM3HUM.PRO
225	-PPLLPEPPDNRSSAPP--RKDVPHR--CSTH...VAQI.G.AF...KYF..LTRDRHLVSLQPAQMHR..RG..LHDSVD.V..RTS	MMP 17P
285	-----MPDP.S--SE.D-AMMLGP.GKTYA...DYV.TVSDS---GPGPLFRYSAL.EG..GNLD--A.V.S--.R	MMP 18P
282	-----DK.---.S.SL...SL.G.T.I..D.FF..-LHPQQV.A.-LF.TK...E.---NRID....H.S	MMP 20P
167	-----G-----RVN.L-----	MMP 21P
271	-----CDARRRLMKRLCP--SS..FCYEFP.PTVA.TPPPP-----TKTRLVPEGRNVTFCG-----	MMP 22P
467	-----EI.K--Q.IV..G.AQI.G.IF...D.FI..TVTPRDKPMG-PL.V.T..E.---EKID.V..A.Q	GELAHUM.PRO
492	GPTGPPTAGPSTATTVPLSPVDD..N--VNI-....AEIGNQLYL..DGKY..FSEGRGSRPQGP...DK.A.---RK.DSVF.E.L	GELBHAM.PRO

342	RDKILVFKDENFWMIRGYAVL PDYPKSIHT-LGFPGRVKKIDAANVCDK-TTRKTYFFVGWCFWDEMTQTMDKGFQQRVVKHFPGISIR	contig 355 long
294	contig 355 short
337	..EVRF..GNKY.AVQ.QN..HG...D.YSSF...RT..H...LSEE-N.G.....ANKY..Y..YKRS..P.Y.KMIAHD....GHK	COLL1HUM.PRO
338	..L.FL..GNQY.ALS..DI.QG...D.-SNY...SS.OA...F---YRS.....NDQF..Y.NQR.F.EP.Y.KSISGA....ESK	COLL2HUM.PRO
343	H.L.FI.RGRK..ALN..DI.EG...K.-SE..L.KE...S...HFE-D.G..LL.S.NQV..Y.DTNHI...DY.RLIEED....GDK	COLL3HUM.PRO
261	-----KRS-NS..K-----	MATRUM.PRO
341	.NQVFL...DKY.L.SNLRPE.N...S-F...NF.....FNP-RFYR...DNQY..Y..RR.M..P.Y.KLIT.N.Q..GPK	METAHUM.PRO
349	K.LVFI..GNQ..A...NE.RAG..RG...PT.R...IS..-EKN.....EDKY...KRN.S.EP..KQIAED....DSK	STO1HUM.PRO
348	..TVFI..GNE..A...NE.QAG..RG...PTIR...S.-EKK.....AADKY...NS.S.EQ...RLIADD...VEPK	STO2HUM.PRO
352	GH-..WF.QGAQY.VYD.EKPVLG-.APL-.E..LVREF--VH..LVWGPEKN.I...R.RDY...HPS.RRV.SPV.R.ATD-WR.VPSE	STO3HUM.PRO
377	GKFVF-..GDKH.VFDEASLE.G...H.-KE..RGLPTD...LFWM-PNG.....R.NKYY..N.ELRAV.SEY.KNIKV-WE..PES	MTM1HUM.PRO
428	GRFVF-..GDRY.LF.EANLE.G..QPL-.SY.LGIPYDR..T.IWWE-P.GH.F..QEDRY...N.E..RG.P.Y.KPISV-WQ..PAS	MTM2HUM.PRO
398	GNFVF-..GNKY.VFKDITLQ.G..HDL-IT..SGIPPHG..S.IWWE-DVG...K.DRY..YS.EMK...P.Y.KPITV-WK..PES	MTM3HUM.PRO

Fig. 3F



A-G: Antisense RNA probe for human MMP 25

H and I: Sense RNA probe for human MMP 25

Arrows in A, B, C, and D highlight cells in the hair follicle that express MMP 25 message

Cell nuclei are counterstained with H33258 in E, F, and G.

Fig. 5

Fig. 36

310	DH..VF..GDRY.VFKDNN.EEG..RPV-SDFS.L.PGG--...	FSWA-HNDR....KDQLY..Y.DH.RH..P.Y.AQSPL-WR.VPST	MMP 17P
356	TQM.HF..GDKV.RYINFMS.GF..KLN-----RSEPNL...	LYW-PLNQ.VFL.K.SGY.QW..LAR.DFSSY.KPIKGL.T.VPNQ	MMP 18P
343	H.L.FI.RGRK..ALN..DI.EG..K-SE..L.KE...S...HFE-D.G..LL.S.NQV..Y.DTNHI...DY.RLIEED....GDK		MMP 20P
174	-----		MMP 21P
323	-Q...HK.GKVY..-----KQCEPLEFSY..-----	YLALGEA.LSI.ANA	MMP 22P
529	EE.AVF.AGNEY.IYSASTLERG..PL-.S..L.PD.QRV...FNWS-KNK...I.A.DKF..YN.VKKK..P...KLIADAMNA.PDN		GELAHUM.PRO
576	SK.LFF.SGRQV.VYT.AS..G--.RRLD-K..LGAD.AQVTG.LR-S-GRG.MLL.S.RRL....VKA.MV.PRSASE.DRM...VPLD		GELBHAM.PRO
425	VDAAFAQK--GFF----FFSRGSTQFEYDIKTKNITRIMRTNT-----WFQCKEP-----		contig 355 long
382	-----		contig 355 short
426	...V.--MKD...----Y.FH.TR.YKF.P...R.LTLQA.S-----N.RKN		COLL1HUM.PRO
424	...V.--QKEH...----HVFS.PRYAF.LIAQRV..VA.G.K-----LN.RYG		COLL2HUM.PRO
431	...VY--EKN.YI----Y.FN.PI....S.WSNR.V.V.PA.S-----ILW.		COLL3HUM.PRO
267			MATRHUM.PRO
429	I..V.-.SKNKYY----Y.FQ..N.....FLLQR..KTLKS.S-----G.		METAHUM.PRO
437	I..V.--EEF...----Y.FT..S.L.F.PNA.KV.HTLKS.S-----LN.		STO1HUM.PRO
436	...VL--QAF...----Y.FS..S...F.PNARMV.H.LKS.S-----LH.		STO2HUM.PRO
436	I.....DADGY----AY.L..RLYWK.F.PVKVKALE-GFPRLVGP.DF.G.A..ANTLL		STO3HUM.PRO
463	PRGS.MGSDEV.----TY.YK.NKYWKFNQKL-KVEPGYPKSALRD.MG.-----PSGGRP-----DEGTEETEVEIIIEVDEEG		MTM1HUM.PRO
514	PKG..LSNDAAY----TY.YK.TKYWK.F.NERL-RMEPGYPKSILRDFMG.Q.HVEPGRPWDVARPPFNPHGGAEPAEGDVG.DGD		MTM2HUM.PRO
484	PQG..VH.EN..----TY.YKEGVL-.IQTRYSRLEPGHPRSILK.DLSG.D---GPTDRVKEGHSP-----DDVD---		MTM3HUM.PRO
395	L.D.MRWSDGA----SY.F..QEYWKVLDGELEVAP-GYPQSTARD.LV.GDSQADGS-----VAAGVDAEGRPAPPGQHDQSR		MMP 17P
429	PS..MSWQDG-----RVY.FK.KVYWRLN-QQLRVEKGYPRNISHN.MH.RPRTIDTTPSGGNTTPS-----		MMP 18P
431	...VY--EKN.YI----Y.FN.PI....S.WSNR.V.V.PA.S-----ILW.		MMP 20P
175	-----		MMP 21P
363	.N-----EGTYTC-----WRRQQRVLTTYSWRVVRVG		MMP 22P
617	L...VLDLQGG.HS----Y.FK.AYYLKLENQSLKSVKFGSIKS--D.LG.		GELAHUM.PRO

Fig. 36

661 THDV...REKAY.CQDR.YW.V.SRS.LN-----QVDQGVVITY---DIL..P.D
GELBHUM.PRO

471 SSFGFDINKEKAHSGGIK-----ILYHKSLSFI-----FGIVHLLKNTS----IYQ
428
426
424
431
267
429
437
436
436
536 GG-----AVSAAVVL PVL.L.LVLAVGLAVFFRRHGTPRLL.C.RSLLDKV
599 GD..AGV..DGSRVVQMEEVARTVNVWV.VPLL.L.CVLGLTYAL.QMQRKGA PRVLL.CKRSIQEWV
548 -----IV..LDNTASTVKAIA.VIPCI.A.CLLVLVYTVFQFKRGTPRHIL.CKRSMQEWV
470 .ED.YEVCSTS-----GASSPPGAPG.VAATML.LLPPL-----PGALWTAQAQALT--L
488 -----GT..TLDTILSATETT-----FEY
175
363
617
661

contig 355 long
contig 355 short
COLL1HUM.PRO
COLL2HUM.PRO
COLL3HUM.PRO
MATRHUM.PRO
METAHUM.PRO
STO1HUM.PRO
STO2HUM.PRO
STO3HUM.PRO
MTM1HUM.PRO
MTM2HUM.PRO
MTM3HUM.PRO
MMP 17P
MMP 18P
MMP 20P
MMP 21P
MMP 22P
GELAHUM.PRO
GELBHUM.PRO

Fig. 3H

stimulated PBL
fetal skin
cartilage
adipose tissue
bone
PBL
ovary
umbilical cord
parotid
thyroid
salivary gland
pancreas
adrenal gland
placenta
spinal cord
fetal liver
fetal brain
cerebellum
brain
trachea
lung
liver
kidney
skin
thymus
stomach
spleen
sm. intestine
colon
bone marrow
uterus
testis
skel. muscle
prostate
mammary gland
heart

Fig. 4